

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120>-MCH Receptor Antagonist

<130> Case2651

<150> JP 11-266278

<151> 1999-09-20

<150> JP 2000-221055

<151> 2000-07-17

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Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly			
35	40	45	
Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala			
50	55	60	
Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile			
65	70	75	80
Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met			
85	90	95	
Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly			
100	105	110	
Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe			
115	120	125	
Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala			
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Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala			
145	150	155	160
Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr			
165	170	175	
Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val			
180	185	190	
Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe			
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Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile			
210	215	220	

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
 225 230 235 240
 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
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 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
 260 265 270
 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
 275 280 285
 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
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 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
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Thr

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TCCACGGTCA TCTTGCTGT GGTGAAGAAG TCCAAGCTAC ACTGGTGCAG CAACGTCCCC	240
GACATCTTCA TCATCAACCT CTCTGTGGTG GATCTGCTCT TCCTGCTGGG CATGCCTTC	300
ATGATCCACC AGCTCATGGG GAACGGCGTC TGGCACTTG GGGAAACCAT GTGCACCCCTC	360
ATCACAGCCA TGGACGCCAA CAGTCAGTTC ACTAGCACCT ACATCCTGAC TGCCATGACC	420

ATTGACCGCT ACTTGGCCAC CGTCCACCCCC ATCTCCTCCA CCAAGTTCCG GAAGCCCTCC 480
 ATGGCCACCC TGGTGATCTG CCTCCTGTGG GCGCTCTCCT TCATCAGTAT CACCCCTGTG 540
 TGGCTCTACG CCAGGCTCAT TCCCTTCCCA GGGGGTGCTG TGGGCTGTGG CATCCGCCCTG 600
 CCAAACCCGG ACACTGACCT CTACTGGTTC ACTCTGTACC AGTTTTCTT GCCCTTGCC 660
 CTTCCGTTG TGGTCATTAC CGCCGCATAC GTGAAAATAC TACAGCGCAT GACGTCTCG 720
 GTGGCCCCAG CCTCCCAACG CAGCATCCGG CTCGGACAA AGAGGGTGAC CCGCACGGCC 780
 ATTGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCCT ACTATGTGCT GCAGCTGACC 840
 CAGCTGTCCA TCAGCCGCC GACCCTCACG TTTGTCTACT TGTACAACGC GGCCATCAGC 900
 TTGGGCTATG CTAACAGCTG CCTGAACCCC TTTGTGTACA TAGTGCTCTG TGAGACCTT 960
 CGAAAACGCT TGGTGTGTC AGTGAAGCCT GCAGCCCAGG GGCAGCTCCG CACGGTCAGC 1020
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 AUCAGCUGUC UGAGCGUUGC UGACCGUGCG GAGCUGCCCC UGGGCUGCAG GCUUCACUGA 180
 CAACACCAAG CGUUUUUCGAA AGGUCUCACA GAGCACUAUG UACACAAAGG GGUUCAGGCA 240
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GGACAAGGTG GCAGGGCGCTG GAGGCTGCCG CAGCCTGCGT GGGTGGAGGG GAGCTCAGCT 180
CGGTTGTGGG AGCAGGCGAC CGGCACTGGC TGGATGGACC TGGAAGCCTC GCTGCTGCC 240
ACTGGTCCA ACGCCAGCAA CACCTCTGAT GGCCCCGATA ACCTCACTTC GGCAGGATCA 300
CCTCCTCGCA CGGGGAGCAT CTCCTACATC AACATCATCA TGCCTCGGT GTTCGGCAC 360
ATCTGCCTCC TGGGCATCAT CGGGAACCTCC ACGGTCACTCT TCGCGGTCGT GAAGAAGTCC 420
AAGCTGCACT GGTGCAACAA CGTCCCCGAC ATCTTCATCA TCAACCTCTC GGTAGTAGAT 480
CTCCTCTTTC TCCTGGGCAT GCCCTTCATG ATCCACCAGC TCATGGCAA TGGGGTGTGG 540
CACTTTGGGG AGACCATGTG CACCCCTCATC ACGGCCATGG ATGCCAATAG TCAGTTCAC 600
AGCACCTACA TCCTGACCGC CATGGCCATT GACCGCTACC TGGCCACTGT CCACCCCCATC 660
TCTTCCACGA AGTTCCGGAA GCCCTCTGTG GCCACCCCTGG TGATCTGCCT CCTGTGGGCC 720
CTCTCCTTCA TCAGCATCAC CCCTGTGTGG CTGTATGCCA GACTCATCCC CTTCCCAGGA 780
GGTGCAGTGG GCTGCGGCAT ACGCCTGCCA AACCCAGACA CTGACCTCTA CTGGTTCAC 840
CTGTACCAGT TTTTCCCTGGC CTTTGCCCTG CCTTTGTGG TCATCACAGC CGCATAACGTG 900
AGGATCCTGC AGCGCATGAC GTCCTCAGTG GCCCCCCGCCT CCCAGCGCAG CATCCGGCTG 960

CGGACAAAGA GGGTGACCCG CACAGCCATC GCCATCTGTC TGGTCTTCTT TGTGTGCTGG 1020
 GCACCCTACT ATGTGCTACA GCTGACCCAG TTGTCCATCA GCCGCCCGAC CCTCACCTTT 1080
 GTCTACTTAT ACAATGCGGC CATCAGCTTG GGCTATGCCA ACAGCTGCCT CAACCCCTTT 1140
 GTGTACATCG TGCTCTGTGA GACGTTCCGC AAACGCTTGG TCCTGTCGGT GAAGCCTGCA 1200
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<212> PRT

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35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala

50 55 60

Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly

65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met

100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser

115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn

130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
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 165 170 175
 Val Trp His Phe Gly Glu Thr MeT Cys Thr Leu Ile Thr Ala MeT Asp
 180 185 190
 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala MeT Ala Ile
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 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
 210 215 220
 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
 225 230 235 240
 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
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 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
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 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Leu Ala Phe Ala Leu
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 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg MeT
 290 295 300
 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
 305 310 315 320
 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
 325 330 335
 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
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 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
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 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys

370 375 380
Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
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TCCACGGTCA TCTTCGCGGT CGTGAAGAAG TCCAAGCTGC ACTGGTGCAA CAACGTCCCC 240

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ATCGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCCT ACTATGTGCT ACAGCTGACC 840

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 CATCTGCCTC CTGGGCATCA TCGGGAACTC CACGGTCATC TTCGCGGTG TGAGAACGTC 420
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GCUGCAGGCU UCACCGACAG GACCAAGCGU UUGCGGAACG UCUCACAGAG CACGAUGUAC 180
ACAAAGGGGU UGAGGCAGCU GUUGGCAUAG CCCAAGCUGA UGGCCGCAUU GUUAAGUAG 240
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GCCCAGCACA CAAAGAAGAC CAGACAGAUG GCGAUGGCUG UGCGGGUCAC CCUCUUUGUC 360
CGCAGCCGGA UGCUGCGCUG GGAGGCGGGG GCCACUGAGG ACGUCAUGCG CUGCAGGAUC 420